## SEQUENCE LISTING

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Leu Pl															222
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Phe Ly	s Leu	Ile	His	Gly	Ser	Gly	Lys	Glu	Glu	Thr	Ser	Lys	Glu	Ala	
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aaa at Lys Il	e Arg					Arg					Leu			_	318
														_	318
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230

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_				act Thr	-		_	-	_			_				510
				ttc Phe	_		_	_								558
	-		-	ata Ile						-		_	-			606
	_			gat Asp					_	_				_		654
				ctc Leu 170		-		-	_	_		_	_			702
		_	-	caa Gln	-	_			_		_			-		750
		-	_	atg Met	_		_		_	_						798
_	_		-	tca Ser			_		_				_			846
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2

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235

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<sup>&</sup>lt;210> 2

<sup>&</sup>lt;211> 235

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115

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Thr	Ser	Lys 35	Glu	Ala	Lys	Ile	Arg 40	Ala	Lys	Glu	Lys	Arg 45	Asn	Arg	Leu
Ser	Leu 50	Leu	Val	Gln	Lys	Pro 55	Glu	Phe	His	Glu	Asp 60	Thr	Arg	Ser	Ser
Arg 65	Ser	Gly	His	Leu	Ala 70	Lys	Glu	Thr	Arg	Val 75	Ser	Pro	Glu	Glu	Ala 80
Val	Lys	Trp	Gly	Glu 85	Ser	Phe	Asp	Lys	Leu 90	Leu	Ser	His	Arg	Asp 95	Gly
Leu	Glu	Ala	Phe 100	Thr	Arg	Phe	Leu	Lys 105	Thr	Glu	Phe	Ser	Glu 110	Glu	Asn
Ile	Glu	Phe	Trp	Ile	Ala	Cys	Glu	Asp	Phe	Lys	Lys	Ser	Lys	Gly	Pro

Gln Gln Ile His Leu Lys Ala Lys Ala Ile Tyr Glu Lys Phe Ile Gln
130 135 140

Thr Asp Ala Pro Lys Glu Val Asn Leu Asp Phe His Thr Lys Glu Val

125

120

145 150 155 160

Ile Thr Asn Ser Ile Thr Gln Pro Thr Leu His Ser Phe Asp Ala Ala 165 170 175

Gln Ser Arg Val Tyr Gln Leu Met Glu Gln Asp Ser Tyr Thr Arg Phe 180 185 190

Leu Lys Ser Asp Ile Tyr Leu Asp Leu Met Glu Gly Arg Pro Gln Arg 195 200 205

Pro Thr Asn Leu Arg Arg Ser Arg Ser Phe Thr Cys Asn Glu Phe 210 215 220

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actgggacag aat atg gat atg tca ctg gtt ttc ttc tct caa tta aat  Met Asp Met Ser Leu Val Phe Phe Ser Gln Leu Asn  1 . 5 10													
atg tgt gaa tca aaa gag aaa act ttt ttc aaa cta atg cat ggg tca 217 Met Cys Glu Ser Lys Glu Lys Thr Phe Phe Lys Leu Met His Gly Ser 15 20 25													
ggg aaa gaa gaa aca agc atc gag gcc aaa atc aga gcg aaa gaa aaa 265 Gly Lys Glu Glu Thr Ser Ile Glu Ala Lys Ile Arg Ala Lys Glu Lys 30 35 40													
agg aat aga cta agt ctt ctc cta cag agg cct gac ttc cat gga gag 313 Arg Asn Arg Leu Ser Leu Leu Gln Arg Pro Asp Phe His Gly Glu 45 50 55 60													
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cct gaa gaa gca gtg aaa tgg gct gaa tca ttt gac aaa ttg ctc tct 409 Pro Glu Glu Ala Val Lys Trp Ala Glu Ser Phe Asp Lys Leu Leu Ser 80 85 90													
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agt gag gag aac att gaa ttt tgg gtc gcc tgt gaa gac ttc aag aaa 505 Ser Glu Glu Asn Ile Glu Phe Trp Val Ala Cys Glu Asp Phe Lys Lys 110 115 120													
tgc aag gaa cct caa caa atc atc cta aaa gca aag gca atc tat gag 553 Cys Lys Glu Pro Gln Gln Ile Ile Leu Lys Ala Lys Ala Ile Tyr Glu 125 130 135 140													

			_		_	-				_			_	ttt Phe 155		601
		-	-		-	_	_		-	_				cac His	_	649
	-	_	•		_	-			_		~	-		gac Asp	_	697
		-		_								_		gaa Glu 		745
_		-	_						_	_		-		ttt Phe		793
		_			gat Asp	-	_		-	-	_			tta Leu 235	tga	841
gtaa	aaagt	ca t	ttgt	tctto	ct tt	tgat	agto	g tat	gtgt	cata	tcta	aaaat	cat .	atact	aatac	901
taat	igtgt	ac t	tcta	aaaat	ca ta	agctt	gtgt	c ata	agaa	agag	atga	attto	cat ·	tttta	aaata	961
cac	catgo	caa a	ataca	atatt	ca aa	atgta	aagaa	a ctt	ttta	atat	tata	actaa	aaa ·	taatt	catca	1021
tcta	atctt	ca q	gaaat	tatti	ct at	gaaa	atct	ato	ctgat	att	ctat	tcta	aat .	aaaat	tcttt	1081
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Ser	Leu 50			Arg	•		-		Thr	Gln	Ala	Ser

25

- Arg Ser Ala Leu Leu Ala Lys Glu Thr Arg Val Ser Pro Glu Glu Ala
  65 70 75 80
- Val Lys Trp Ala Glu Ser Phe Asp Lys Leu Leu Ser His Arg Asp Gly 85 90 95
- Val Asp Ala Phe Thr Arg Phe Leu Lys Thr Glu Phe Ser Glu Glu Asn 100 105 110  $\cdots$
- Ile Glu Phe Trp Val Ala Cys Glu Asp Phe Lys Lys Cys Lys Glu Pro 115 120 125
- Gln Gln Ile Ile Leu Lys Ala Lys Ala Ile Tyr Glu Lys Phe Ile Gln 130 135 140
- Ile Ala Lys Ser Ile Ala Gln Pro Thr Leu His Ser Phe Asp Thr Ala 165 170 175
- Gln Ser Arg Val Tyr Gln Leu Met Glu His Asp Ser Tyr Lys Arg Phe 180 185 190
- Leu Lys Ser Glu Thr Tyr Leu His Leu Ile Glu Gly Arg Pro Gln Arg 195 200 205
- Pro Thr Asn Leu Arg Arg Ser Arg Ser Phe Thr Tyr Asn Asp Phe 210 215 220
- Gln Asp Val Lys Ser Asp Val Ala Ile Trp Leu 225 230 235